

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	605.5	46.9	247	7	US-11-330-403-4637	Sequence 4637, Ap		
2	517.5	40.1	309	6	US-10-603-113-16823	Sequence 16823, A		
3	513	39.8	253	7	US-11-330-403-17429	Sequence 17429, A		
4	482	37.4	244	7	US-11-330-403-14243	Sequence 14243, A		
5	457.5	35.5	261	7	US-11-314-869-74	Sequence 74, Appl		
6	450	34.9	252	6	US-10-573-130B-4	Sequence 4, Appli		
7	444	34.4	246	7	US-11-330-403-14990	Sequence 14990, A		
8	441.5	34.2	322	7	US-11-637-782-128	Sequence 128, App		
9	441.5	34.2	324	7	US-11-637-782-15	Sequence 15, Appl		
10	441.5	34.2	520	7	US-11-634-921-11	Sequence 11, Appl		
11	441.5	34.2	727	7	US-11-634-921-128	Sequence 128, App		
12	434.5	33.7	261	6	US-10-975-697-6	Sequence 6, Appli		
13	434.5	33.7	261	7	US-11-559-607-6	Sequence 6, Appli		
14	434.5	33.7	267	6	US-10-975-697-14	Sequence 14, Appl		
15	434.5	33.7	267	7	US-11-559-607-14	Sequence		

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

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SUMMARIES

Result No.	% Query						Description
	Score	Match	Length	DB	ID		
1	605.5	46.9	247	7	US-11-330-403-4637		Sequence 4637, Ap
2	517.5	40.1	309	6	US-10-603-113-16823		Sequence 16823, A
3	513	39.8	253	7	US-11-330-403-17429		Sequence 17429, A
4	482	37.4	244	7	US-11-330-403-14243		Sequence 14243, A
5	457.5	35.5	261	7	US-11-314-869-74		Sequence 74, Appl
6	450	34.9	252	6	US-10-573-130B-4		Sequence 4, Appli
7	444	34.4	246	7	US-11-330-403-14990		Sequence 14990, A
8	441.5	34.2	322	7	US-11-637-782-128		Sequence 128, App
9	441.5	34.2	324	7	US-11-637-782-15		Sequence 15, Appl
10	441.5	34.2	520	7	US-11-634-921-11		Sequence 11, Appl
11	441.5	34.2	727	7	US-11-634-921-128		Sequence 128, App
12	434.5	33.7	261	6	US-10-975-697-6		Sequence 6, Appli
13	434.5	33.7	261	7	US-11-559-607-6		Sequence 6, Appli
14	434.5	33.7	267	6	US-10-975-697-14		Sequence 14, Appl
15	434.5	33.7	267	7	US-11-559-607-14		Sequence

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/iaa/backfiles1.pep:*

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SUMMARIES

		%					Description
Result	Query	No.	Score	Match	Length	DB ID	
<hr/>							
1	944	73.2	254	2	US-09-978-758-2	Sequence 2, Appli	
2	944	73.2	254	3	US-10-766-421-2	Sequence 2, Appli	
3	573.5	44.5	257	2	US-09-543-681A-6362	Sequence 6362, Ap	
4	517.5	40.1	309	2	US-09-248-796A-16823	Sequence 16823, A	
5	460.5	35.7	261	3	US-10-639-159-12	Sequence 12, Appl	
6	460.5	35.7	261	3	US-10-782-258-12	Sequence 12, Appl	
7	457.5	35.5	261	3	US-09-971-536-74	Sequence 74, Appl	
8	456.5	35.4	261	2	US-10-004-115B-36	Sequence 36, Appl	
9	443.5	34.4	261	3	US-10-639-159-68	Sequence 68, Appl	
10	443.5	34.4	261	3	US-10-782-258-68	Sequence 68, Appl	
11	443	34.3	252	2	US-08-822-322-8	Sequence 8, Appli	
12	443	34.3	252	2	US-09-466-109-8	Sequence 8, Appli	
13	441.5	34.2	261	2	US-09-468-738A-29	Sequence 29, Appl	
14	441.5	34.2	261	2	US-09-940-019-29	Sequence 29, Appl	
15	441.5	34.2	261	2	US-09-940-037A-29	Sequence 29, Appl	
16	441.5	34.2	261	2	US-09-305-390-18	Sequence 18, Appl	
17	441.5	34.2	261	2	US-09-855-309-29	Sequence 29, Appl	
18	441.5	34.2	261	3	US-10-639-159-10	Sequence 10, Appl	
19	441.5	34.2	261	3	US-10-782-258-10	Sequence 10, Appl	
20	441	34.2	250	3	US-10-528-000-1	Sequence 1, Appli	
21	438.5	34.0	261	3	US-10-639-159-64	Sequence 64, Appl	

SUMMARIES

Result No.	% Query		Match Length DB ID			Description
	Score					
1	1290	100.0	254	4	AAB49773	Aab49773 Protein w
2	944	73.2	254	4	AAB47522	Aab47522 (R)-2-oct
3	944	73.2	254	9	AED95198	Aed95198 Propargyl
4	575.5	44.6	248	6	ADB06934	Adb06934 Alloiococ
5	575.5	44.6	281	6	ADB06936	Adb06936 Alloiococ
6	573.5	44.5	257	7	ADF06077	Adf06077 Bacterial
7	556.5	43.1	246	8	ADN17584	Adn17584 Bacterial
8	488.5	37.9	261	6	ABU29919	Abu29919 Protein e
9	467	36.2	264	6	ABP60424	Abp60424 Lactobaci
10	465.5	36.1	272	3	AAB10740	Aab10740 B. megate
11	465.5	36.1	340	3	AAB10741	Aab10741 H. ghilia
12	464.5	36.0	261	2	AAR27756	Aar27756 NAD affin
13	461.5	35.8	261	10	AEI82096	Aei82096 B. lichen
14	460.5	35.7	261	8	ADJ98070	Adj98070 Glucose d
15	460.5	35.7	261	9	ADY81462	Ady81462 Bacillus
16	460.5	35.7	261	9	ADZ77251	Adz77251 Bacillus
17	459.5	35.6	261	1	AAP80063	Aap80063 Glucose d
18	458.5	35.5	261	1	AAP80590	Aap80590 Sequence
19	458.5	35.5	261	8	ADS27701	Ads27701 Bacterial
20	458.5	35.5	261	9	ADZ77299	Adz77299 Bacillus
21	457.5	35.5	261	5	AAE20115	Aae20115 Lactobaci
22	457.5	35.5	261	10	AEG78032	Aeg78032 Aldonic a
23	456.5	35.4	261	5	ABB77971	Abb77971 Amino aci
24	456.5	35.4	261	7	ADE39638	Ade39638 Bacillus
25	456.5	35.4	261	8	ADL18267	Adl18267 Bacillus
26	456.5	35.4	261	8	ADK70264	Adk70264 Bacillus
27	456.5	35.4	261	8	ADK82553	Adk82553 Isomerase

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	No.	Score	Match	Length	DB ID	
1	466.5	36.2	261	2	I40225	glucose 1-dehydrog	
2	465.5	36.1	261	1	S00812	glucose 1-dehydrog	
3	460.5	35.7	261	2	I40224	glucose 1-dehydrog	
4	457.5	35.5	261	2	JS0385	glucose 1-dehydrog	
5	457.5	35.5	261	2	I39853	glucose 1-dehydrog	
6	451.5	35.0	261	2	A33528	glucose 1-dehydrog	
7	441.5	34.2	261	2	D69629	glucose 1-dehydrog	
8	437	33.9	262	2	S02299	glucose 1-dehydrog	
9	434.5	33.7	263	2	S01227	glucose 1-dehydrog	
10	418	32.4	272	2	AG3359	glucose 1-dehydrog	
11	410.5	31.8	255	1	S39737	glucose 1-dehydrog	
12	407.5	31.6	245	2	AE3517	3-oxoacyl-(acyl-ca	
13	393.5	30.5	299	2	D90481	hypothetical prote	
14	390.5	30.3	269	2	AE2285	glucose 1-dehydrog	
15	386.5	30.0	258	2	G69755	glucose 1-dehydrog	

Listing first 45 summaries

Database : UniProt_8.4:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score						
1	605.5	46.9	247	2	Q81AU6	BACCR	Q81au6 bacillus ce
2	550	42.6	246	2	Q8G0H2	BRUSU	Q8g0h2 brucella su
3	522.5	40.5	262	2	Q5A1C0	CANAL	Q5a1c0 candida alb
4	513	39.8	253	2	Q46PX5	RALEJ	Q46px5 ralstonia e
5	494	38.3	261	2	Q41AP4	9BACI	Q41ap4 exiguobacte
6	489.5	37.9	261	2	Q3XZ55	ENTFC	Q3xz55 enterococcu
7	489.5	37.9	262	2	Q5FK32	LACAC	Q5fk32 lactobacill
8	489	37.9	251	2	Q1U7C8	LACRE	Q1u7c8 lactobacill
9	487	37.8	251	2	Q2BUL7	LACRE	Q2bul7 lactobacill
10	482	37.4	244	2	Q8ELC2	OCEIH	Q8elc2 oceanobacil
11	474	36.7	252	2	Q6WVP7	9LACO	Q6wvp7 lactobacill
12	466.5	36.2	261	1	DHG4	BACME	P39485 bacillus me
13	466.5	36.2	264	2	Q1WVF6	LACS1	Q1wvf6 lactobacill
14	465.5	36.1	261	1	DHGA	BACME	P10528 bacillus me
15	461.5	35.8	261	2	Q9F2A6	BACLI	Q9f2a6 bacillus li
16	461.5	35.8	261	2	Q65HM4	BACLD	Q65hm4 bacillus li
17	460.5	35.7	261	1	DHG3	BACME	P39484 bacillus me
18	460.5	35.7	261	2	Q3EU76	BACTI	Q3eu76 bacillus th